CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/671,953B   ENTERED   CRF Processing Date: 11/7/2002
Edited by:
Verified by: _____ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII

- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- ☐ Edited a format error in the Current Application Data section, specifically: _____

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

- ☐ Added the mandatory heading and subheadings for "Current Application Data".

- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- ☐ Inserted colons after headings/subheadings. Headings edited included: _____

- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

- ☑ Inserted mandatory headings, specifically: <220> in Sequences 17,21

- ☐ Corrected an obvious error in the response, specifically: _____

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

- ☐ Corrected an error in the Number of Sequences field, specifically: _____

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- ☐ Other: _____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

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DEC 1 2 2002

TECH CENTER 1600/2900

1600

```
          RAW SEQUENCE LISTING                    DATE: 11/07/2002
          PATENT APPLICATION:  US/09/671,953B     TIME: 20:55:42

          Input Set : A:\PTO.AMC.txt
          Output Set: N:\CRF4\11072002\I671953B.raw          P.6
```

```
 3 <110> APPLICANT: Meares, Claude
 4         Chmura, Albert
 5         The Regents of the University of California
 7 <120> TITLE OF INVENTION: Engineering Antibodies That Bind Irreversibly
 9 <130> FILE REFERENCE: 023070-099120US
11 <140> CURRENT APPLICATION NUMBER: US 09/671,953B
12 <141> CURRENT FILING DATE: 2000-09-27
14 <150> PRIOR APPLICATION NUMBER: US 60/156,194
15 <151> PRIOR FILING DATE: 1999-09-27
17 <150> PRIOR APPLICATION NUMBER: US 60/208,684
18 <151> PRIOR FILING DATE: 2000-05-31
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 753
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
31         that encodes Fab heavy chain of CHA255
33 <400> SEQUENCE: 1
34 agatctgaag tgacgctggt ggagtctagg ggagactcag tgaagcctgg agggttcctg 60
35 aaactctcct gtgcagcctc tggattcact ttaagtggtg aaaccatgtc ttgggttcgc 120
36 cagactccgg agaagaggct ggagtgggtc acaaccactc ttagtggtgg tggtttcacc 180
37 ttctattcag ccagtgtgaa gggtcgtttc accatctcca gagacaatgc ccagaacaac 240
38 ctctatctac aactgaatag tctgaggtct gaggacacgg ccttgtattt ctgtgcaagt 300
39 catcggtttg ttcactgggg ccacgggact ctggtcactg tctctgcagc caaaacgacg 360
40 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
41 ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480
42 gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcaag actctacttc 540
43 ctcagcagcg tggtgaccgt gcccttcaac agcttgggca cccagaccta catctgcaac 600
44 gtgaatcaca gcccagcaa caccaaggtg gacaagaaag cagagcccaa atcttgtgac 660
45 aaatctagag ggcccttcga aggtaagcct atccctaacc ctctcctcgg tctcgattct 720
46 acgcgtaccg gtcatcatca ccatcaccat tga                             753
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 657
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
56         that encodes light chain mutant with Cys
57         substituted for Asn at position 97 of CHA255
59 <400> SEQUENCE: 2
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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11072002\I671953B.raw

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60 agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctggtga aacagtcaca 60
61 ctcacttgtc gctcaagtat tggggctgtt acaactagta actatgccaa ctgggtccaa 120
62 gaaaaaccag atcatttatt cactggtcta ataggtggta ccaataaccg ggctccgggt 180
63 gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
64 gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactcctg cctctgggtr 300
65 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
66 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
67 aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
68 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
69 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
70 acccatcagg gcctgagyty gcccgtcaca aagagcttca cagggagga gtgttaa    657
```

73 <210> SEQ ID NO: 3
74 <211> LENGTH: 657
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
80   that encodes the unmodified light chain of CHA255
82 <400> SEQUENCE: 3

```
83 agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctggtga aacagtcaca 60
84 ctcacttgtc gctcaagtat tggggctgtt acaactagta actatgccaa ctgggtccaa 120
85 gaaaaaccag atcatttatt cactggtcta ataggtggta ccaataaccg ggctccgggt 180
86 gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
87 gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactccaa cctctgggtr 300
88 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
89 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
90 aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
91 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
92 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
93 acccatcagg gcctgagyty gcccgtcaca aagagcttca cagggagga gtgttaa    657
```

96 <210> SEQ ID NO: 4
97 <211> LENGTH: 657
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
103   that encodes light chain mutant with Cys
104   substituted for Ser at position 96 of CHA255
106 <400> SEQUENCE: 4

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107 agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctggtga aacagtcaca 60
108 ctcacttgtc gctcaagtat tggggctgtt acaactagta actatgccaa ctgggtccaa 120
109 gaaaaaccag atcatttatt cactggtcta ataggtggta ccaataaccg ggctccgggt 180
110 gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
111 gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactgcaa cctctgggtr 300
112 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
113 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
114 aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
115 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
116 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
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RAW SEQUENCE LISTING   DATE: 11/07/2002
PATENT APPLICATION: US/09/671,953B   TIME: 20:55:42

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11072002\I671953B.raw

117 acccatcagg gcctgagyty gcccgtcaca aagagcttca acagggagaa gtgttaa   657
120 <210> SEQ ID NO: 5
121 <211> LENGTH: 218
122 <212> TYPE: PRT
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
127   sequence of mutant light chain with Cys
128   substituted for Asn at position 97 of CHA255
130 <220> FEATURE:
131 <221> NAME/KEY: MOD_RES
132 <222> LOCATION: (207)
133 <223> OTHER INFORMATION: Xaa = any amino acid
135 <400> SEQUENCE: 5
136 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
137 1   5   10   15
139 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
140   20   25   30
142 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
143   35   40   45
145 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
146   50   55   60
148 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
149 65   70   75   80
151 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Ser
152   85   90   95
154 Cys Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
155   100   105   110
157 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
158   115   120   125
160 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
161   130   135   140
163 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
164 145   150   155   160
166 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
167   165   170   175
169 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
170   180   185   190
W--> 172 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
173   195   200   205
175 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
176   210   215
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 218
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
186   sequence of unmodified light chain of CHA255

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/671,953B

DATE: 11/07/2002
TIME: 20:55:42

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11072002\I671953B.raw

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188 <220> FEATURE:
189 <221> NAME/KEY: MOD_RES
190 <222> LOCATION: (207)
191 <223> OTHER INFORMATION: Xaa = any amino acid
193 <400> SEQUENCE: 6
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195  1               5                   10                  15
197 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
198              20                  25                  30
200 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
201          35                  40                  45
203 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
204          50                  55                  60
206 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
207  65                  70                  75                  80
209 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Ser
210              85                  90                  95
212 Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
213              100                 105                 110
215 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
216              115                 120                 125
218 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
219          130                 135                 140
221 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
222 145                 150                 155                 160
224 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
225              165                 170                 175
227 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
228              180                 185                 190
W--> 230 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
231          195                 200                 205
233 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
234          210                 215
237 <210> SEQ ID NO: 7
238 <211> LENGTH: 218
239 <212> TYPE: PRT
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
244          sequence of mutant light chain with Cys
245          substituted for Ser at position 96 of CHA255
247 <220> FEATURE:
248 <221> NAME/KEY: MOD_RES
249 <222> LOCATION: (207)
250 <223> OTHER INFORMATION: Xaa = any amino acid
252 <400> SEQUENCE: 7
253 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
254  1               5                   10                  15
256 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
```

RAW SEQUENCE LISTING   DATE: 11/07/2002
PATENT APPLICATION: US/09/671,953B   TIME: 20:55:42

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11072002\I671953B.raw

```
257                20                    25                    30
259 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
260             35                    40                    45
262 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
263       50                    55                    60
265 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
266 65                    70                    75                    80
268 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Cys
269             85                    90                    95
271 Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
272             100                   105                   110
274 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
275       115                   120                   125
277 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
278       130                   135                   140
280 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
281 145                   150                   155                   160
283 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
284             165                   170                   175
286 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
287             180                   185                   190
W--> 289 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
290             195                   200                   205
292 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
293       210                   215
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296 <210> SEQ ID NO: 8
297 <211> LENGTH: 250
298 <212> TYPE: PRT
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
303   sequence of unmodified heavy chain of CHA255
305 <400> SEQUENCE: 8

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306 Arg Ser Glu Val Thr Leu Val Glu Ser Arg Gly Asp Ser Val Lys Pro
307 1                 5                     10                    15
309 Gly Gly Phe Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
310             20                    25                    30
312 Gly Glu Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu
313             35                    40                    45
315 Trp Val Thr Thr Thr Leu Ser Gly Gly Gly Phe Thr Phe Tyr Ser Ala
316       50                    55                    60
318 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Asn
319 65                    70                    75                    80
321 Leu Tyr Leu Gln Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr
322             85                    90                    95
324 Phe Cys Ala Ser His Arg Phe Val His Trp Gly His Gly Thr Leu Val
325             100                   105                   110
327 Thr Val Ser Ala Ala Lys Thr Thr Gly Pro Ser Val Phe Pro Leu Ala
328       115                   120                   125
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/07/2002
PATENT APPLICATION: US/09/671,953B   TIME: 20:55:43

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11072002\I671953B.raw

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 207
Seq#:6; Xaa Pos. 207
Seq#:7; Xaa Pos. 207
Seq#:20; N Pos. 405